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ALIGNMENTS

LOCUS DEFINITION JOURNAL MEDLINE PUBMED ORGANISM AUTHORS MEDLINE PUBMED Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayatsizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000) Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253 Mus musculus Eukaryota; Metazoa; Mammalia; Eutheria; HTC; CAP trapper.

Mus musculus (strain:C57BL/6J) 16 days embryo lung cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library AK018423 2125 bp mRNA linear HTC 19-7AN-200 Mus musculus 16 days embryo lung cDNA, RIKEN full-length enriched library, clone:8430417G17:similar to ILEAL NA+-DEPENDENT BILE ACITRANSPORTER (ISBT), full insert sequence. clone:8430417G17. AK018423.1 GI:12858114 AK018423 11042159 20499374 Chordata; Rodentia; Craniata; Vertebrata; Euteleosto Sciurognathi; Muridae; Murinae; Vertebrata; Euteleostomi; HTC 19-JAN-2002 Mus. ACID genes

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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Brai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Carninci, P., Irokuda, S., Fukunishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
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DNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.2. Second Strand cDNA was prepared with the primer
                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemonic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further derails
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wyDSTGITLVSLVVPVASGVVVNYRWPKQAGVTISIETGAQNIQLCIAMLQKS
SAEYLVQLLMFALAYGLFQVLHGLLLVAAYQAYKRRQKSKCRRQHPDCPDVCYEKQP
RETSAFLDKGDEAAVTLGPVQPEQHHRAAELTSHIPSCE"
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/dev stage="16 days embryo"
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                                                                         Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                                                                                        1 (bases 1 to 652)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Koud,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasak,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagama,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y., RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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                                                                             Yokohama, Kanagawa 230-0045, Japan
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Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome to (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e mouse tissues.
GCCTGCTTTCCCAGTTTGGACTTATGCCTCTGACAGCTTATCTGTTAGCCATTGGCTTCG
                                            GACTGCTCTGCCAGTTTGGGCTCATGCCTTTTACAGCTTATCTCCTGGCCATTAGCTTTT
                                                                                                                                                 GTTCCGTGGAGATCCGGAAGCTGTGGTCGCACATCAGGAGACCCTGGGGCATTGCTGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Site 1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primed with a primer [5' GAGAGAGAGAGAGAGAGATOVA 3'], cDNA was
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| dab_host="DH10B"
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lone="4831431E11"
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81.7%;
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Pred. No. 2.8e-119;
D; Mismatches 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
BG872314
BG872314.1 GI:
EST.
                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10841 row: j column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 972)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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602790977F1 NCI_CGAP_SG2
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGTGTGGTCCTGGCGAAAGGATCTTGGAATTCAGACATCACCCTTCTGACCATCAGTT
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     222
                                                                                                                                                                                                       quality sequence stop: 786.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:492227"
/clone="imaGE:492227"
/clone=ib="NCI_CGAP_SG2"
/lab_host="DHIOB (T1_phage-resistant)"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_Not1; Site_2: Sali; Cloned unidirectionally. Primer: Oli dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
a 277 c 263 g 210 t
                                                                                                                                                       strain="FVB/N"
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Matches 458; Conserv
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                                                              1 (bases 1 to 356)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Roldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                          BE181226 356 bp mRI
CM2-HT0630-220300-125-f05 HT0630 Homo
BE181226
                               Shotgun sequencing of the human transcriptome with ORF
                                                 Simpson, A.J.
                                                                                                                                                                                                                                                          BE181226.1
              sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutėleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 658)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
                                                       Mus musculus
                                                                                                               BB625035.1 GI:16463388
                                                                             nouse mouse.
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/db_xref="taxon:9606"
/clone_lib="HT0630"
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No. 1e-83;
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   149
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
uayashiratio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., e Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
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e mouse tissues.
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rom Lambda
BamHI"
                           /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                        contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="9030619K19"
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lab_host="DH10B"
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Best Local Similarity
Matches 317; Conserv
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                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 662)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y., RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group,
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (R
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus
BB664585
                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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RIKEN full-length enriched, 0 day neonate lung Mus
cDNA clone E030047A18 5', mRNA sequence.
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Pred. No. 1.1e-46;
0; Mismatches 195;
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Best Local
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199
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Carninci,P., Shibata,Y., Hayateu,N., Sugahara,Y., Shibata,K., It
Carninci,P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuu
N.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizaw,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Please visit our web further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Genome Sequences. Mamm.
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sug
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                                                                                                                                                                                                          CCAGTGGGACTGGAGGTGCATGGAAACCTGGAGCTCGTTTTCACAGTGGTGTCCACTGTG
                                          CACATCAGGAGACCCTGGGGCATTGCTGTGGGACTGCTCTGCCAGTTTGGGCTCATGCCT
                                                                                                                                                                                                                                                                                               CACCTCAGAAGACCCTGGGCATGGCACTGGGCCTGGTTTCGCAGGTTGGATTTATGCCT
                                                                                                                                ATGATGGGGCTGCTCATGTTCTCTTTGGGATGTTCCGTGGAGATCCGGAAGCTGTGGTCG
                                                                                                                                                                            CCCGTGGGAATGGAGGACATGCGAATCTAATGCTGCTTTTTACAGTGCTATCCGCTGTG
                                                                                                                                                                                                                                                                       AAGAGCACAGACTGTGCGGGCAACTCCACCAGCCCTGTGAACAGTGCGGAGGAAGACCCG
                                                                                        ÁTGGTGGGGGGGTAATGCTCACTTTTGGATGTAGAGCGGACAGTGAGAATCTCTGGTTG

    Conservative

                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5, GAGAGAGATTCAGATTAATTAATCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="E030047A18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="0 day neonate"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="lung"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone_lib="RIKEN full-length"
                                                                                                                                                                                                                                                                                                                                                                            17.6%;
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                                                                                                                                                                                                                                                                                                                                                           Score 200; DB 10;
Pred. No. 1.1e-46;
0; Mismatches 110;
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VERSION
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 289
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                                                                                                                                                                                             109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU176916 Sugano-Kawakami 5' end enriched cDNA library (CLA) from HNI Oryzias latipes cDNA clone OLAZZ:10c similar to pir [A49876] Na+-dependent bile acid transporter, ileal - golden hamster, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Kiyoshi Naruse
Department of Biological Sciences
Graduate School of Science, Unive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 81-3-5841-4443
Fax: 81-3-5841-4410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hongo 7-3-1, Bunkyo-ku,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Naruse, K., Mitani, H. and Tanaka, M. Medaka EST Project in University of Tokyo (2001)
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                                                                                                                                                                                                                                            Similarity
 GCTATTGCTGTTCTCATCATGGGCTGCCGGGGGGGCACCATCTCTAACATTTTCACC 348
                                                              GGGCTCATGCCTTTTACAGCTTATCTCCTGGCCATTAGCTTTTCTCTGAAGCCAGTCCAA 288
                                                                                                               AAGCTGTGGTCGCACATCAGGAGACCCTGGGGCATTGCTGTGGGACTGCTCTGCCAGTTT
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                                                                                                                                                                                                                                                                                                            106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l: naruse@biol.s.u-tokyo.ac.jp
clone was isolated from Sugano-Kawakami 5'
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                         /tissue_type="whole body"
/dev_stage="adult"
200 c 167 g 169
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11518 row: k column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
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Mammalia; Eutheria;
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                                                                                                                                                       Similarity
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                                                                                                                                   Conservative
                                                                                                                                                                                                                          /note-"Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db_xref="taxon:9606"
'clone="IMAGE:5206781"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="NIH_MGC_122"
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                                                                                                                               Score 189; DB 1
Pred. No. 1.7e-4
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                                                                                                                                                                                                                                   This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM2-HT0285-081 199-028-a09&t3=1999-11-08&t4=1)  
Seq primer: puc 18 forward the primer is puc 18 forward the puc 18 forwa
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1 (bases 1 to 274)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Baia,G.S., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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CM2-HT0285-081199-028-a09
BE151388 GI:8614109
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: +55-11-2704922
Fax: +55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                                                                                       Email: asimpson@ludwig.org.br
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/db_xref="taxon:9606"
/clone_lib="HT0285"
                                organism="Homo sapiens"
/db_xref="taxon:9606"
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REFERENCE
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                                                                                                                                                                     Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For
Clones are derived from the human BAC library RPCI-11. For
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased f
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering)
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_sear
                                                                                                                                                                                                                                                                                                                        Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
Other_GSSs: RPCI11-2407.TKBR
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Use of BAC End Sequences for
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Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.
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/clone_lib="RPCI-11"
/sex="Male"
                                   /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="RPCI-11-2407"
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                        USDA, ARS, US Meat
PO Box 166, Clay Co
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 538)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A.,
                                                                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                                                                                    FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE030429.1
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                                                                                                                                                                                                                                                                                                       PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCCTTTGATTGGCCATGTCACGGGTTTTCTGCTGGCACTTTTTTACCCACCAGTCTTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCTCAAGATTGGGGCCGTTGTTGGTGGGGGTCCTTCTTGGTGGTCGCAGTTGCTGGTG
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                                                                                                                                                                                                               te: 58 row: A column: 1
primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                         ARS, US Meat Animal Research Center
x 166, Clay Center, NE 68933-0166, USA
                                                                                                             /organism="Sus scrofa"
/db xref="taxon:9823"
/clone_lib="MARC_1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
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                                             Library made from pooled tissue and 30 embryos."
142 c 153 g 136 t
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RPCI11 Human Male BAC Library"
118 c 97 g 160 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="Lymphocytes"
/note="Vector: pBACe3.6;
                                                                                                  note="Vector:
                                                                                                                                                                                                   .538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:8325438
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95.4%;
 14.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E
on, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
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Pred. No. 1.1
 Score 164.6;
                                                                               pCMV SPORT6; Site 1: NotI; Site 2: rom pooled tissue from day 11, 13, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       686 bp mRNA linear EST 20-(um18f05.yl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2192673 5' similar to TR:P70172 P70172 ILEAL NA+-DEPEN BILE ACID TRANSPORTER ;, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 686)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Thelsing,B., Allen,M., Bowers,Y., Pe,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ri, Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                          Seq primer: custom primer used High quality sequence stop: 49:
                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-
                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa,
Mammalia, Eutheria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW107022.1
                                                                                                                                                                                                                                                                                                      MGI:1005125
                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCATGGGCTGCCGGGGGGGGCACCATCTCTAACATTTTCACCTTCTGGGTTGATGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAGGAGACCCTGGGGCATTGCTGTGGGGACTGCTCTTGCCCAGTTTTGGGCTCATGCCTTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGGGCTGCTCATGTTCTCTTTGGGATGTTCCGTGGAGATCCCGGAAGCTGTGGTCGCACA 184
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/dev_stage="adult"
/lab_host="H10B"
/note="Organ: kidney; Vector: pME18
/note="Organ: kidney; Vector: CACCAT
(CACTGTGTG); Site 2: DraIII (CACCAT
was primed with an oligo(dT) primer
                                                                                                                                                                                                                       1. .686
                                                                                                                                                                                                                                       cocation/Qualifiers
                                                                                                                  /db_xref="taxon:10000"
/clone="IMAGE:2192673"
/clone=lib="Sugano mouse
                                                                                                    sex="female"
                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                                   strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.3%;
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0; Mismatches 99;
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                                                                                                                           kidney mkia"
                    : pME18S-FL3; Site_1: DraIII
(CACCATGTG); 1st strand cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                         Louis, MO
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Schurk, R., Ritter
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JOURNAL COMMENT
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                 1 (bases 1 to 666)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Noura, K., Ohno, M., Sasaki, D., Shibata, K., Salo, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagamai, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                      BB625042 RIKEN full-length enriched, adult cDNA clone 9030621119 5', mRNA sequence. BB625042 BB625042.1 GI:15398453
                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                         house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTACACCAAGATGTGGGGTTGACTCGTGAACGATTGTGATTCACTATGATAGCATTGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTACACCTGGTCCTGGAGTCTTCAGCAGAATCTCACCATTCCTTATCAGAACATAGGAA 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  þ
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  Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [ATCTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DrailI adaptor [TTTGGCCTACTGG], digested and cloned into distinct DrailI sites of the pME18S-FL3 vector [5' site CACTGTGTG, 3' site CACCATGTG) Xhol should
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Pred. No. 8.7e-36;
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Best Local Similarity
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185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Yamanaka, I. Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizaw, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T. Ishii, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001 Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           further details
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                                                ATGGAAACCTGGAGCTCGTTTTCACAGTGGTGTCCACTGTGATGATGGGGGCTGCTCATGT 139
ATGCAATTCTCAATACAGTGATGAGCACTGTGCTCACCATCCTCTAGCCATGGTGATGT
                                                                                                                                                                                                                                             147
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                                                                                                                                                                                                                                                                                                                                                                      from Lambda
BamHI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                            Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contributed to prepare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Site_1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="colon"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                          ]. cDNA was cloned into the XhoI and BamHI sites.
ctor: a modified pBluescript KS(+) after bulk excision
om Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                                                                                                                                                                                                                                                146 c
                                                                                                                                  13.2%;
                                                                                                Pred. No. 5.16
0; Mismatches
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                                                                                                                                  Score 149.4; DB 1
Pred. No. 5.1e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse tissues. 1st strand cDNA was
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                                                                                                                                                           DB 10;
                                                                                                                                                           Length
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REFERENCE
AUTHORS
TITLE
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BI149148
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                                                         289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information

found through the I.M.A.G.E. Consortium/LLNL at:
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National Institutes of Health, Mammalian
Unpublished (1999)
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/clone="IMACE:5053578"
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/clone="ImBLOE: CGAP_Li9"
/lab host="NH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
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                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTATGTTGCTGCTCATCATGCTCTCGCTTGGCTGCACCATGGAGTTCAGCAAGATCAAG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATGGAGATATGGATCTCAGCATCAGTATGACAACCTGTTCCACCGTGGCCGCCCTGGGA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTCTCATCATGGGCTGCTGCCCGGGGGGCACCATCTCTAACATTTTCACCTTCTGGGTT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTTTTACAGCTTATCTCCTGGCCATTAGCTTTTCTCTGAAGCCAGTCCAAGCTATTGCT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGCACATCAGGAGACCCTGGGGCATTGCTGTGGGACTGCTCTGCCAGTTTGGGCTCATG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTGTTGGTGGGGTCCTCCTTCTGGTGGTCGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGGTGCCCTACAAAGGCATTATGTTATCACTCGTCATGGTTCTCATTCCTTGCGCCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGATGCCACTCTGCATTTATCTCTACACCT---GGTCCTGGAGTCTTCAGCAGAATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGGGGGACATGAACCTCAGCATTGTGATGACCACCTGCTCCAGCTTCACTGCCTTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCCTCATCTGCGGCTGCTCCTGGGGGGGAACCTGTCTAACCTCTTCACCCTGGCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCCTCAGTGCTTTCCTTGGGCAAGGTCTTTCATCTGACCAGCATTGAGGCTCTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGTCTATGTGAATTACAGATGGCCAAAACAATCCAAAATCATTCTCAAGATTGGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCATTCCTTATCAGAACATAGGAATTACCCTTGTGTGCCTGACCATTCCTGTGGCCTTT 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGATGCCTCTCTTATACATCTACAGCAAAGGAATCTACGACGGAGATCTTAAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 876)
/strain="FVB/N"
/db xref="taxon:10090"
/db xref="taxon:10090"
/clone="IMAGE:4163893"
/clone_lib="NCI_CGAP_Li9"
/clone_lib="NCI_CGAP_Li9"
/lab host="DH10B_(Tl_phage-resistant)"
/lab host="DH10B_(Tl_phage-resistant)"
/note="Organ: liver; Vector: pcMV-SPORT6; Site_l: Notl;
/note="Organ: liver; Vector: pcMV-SPORT6; Site_l: Notl;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                           location/Qualifiers
                                                                                                                                      organism="Mus musculus"
                                                                                                                                                     .876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:11146527
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Rodentia;
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Mus
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thi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                        Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear EST 14-NOV-2000 clone IMAGE:4163893 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                          (MGC)
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.5%; Score 141.2; DB 12; Length 876; Best Local Similarity 55.9%; Pred. No. 1.3e-29; Matches 288; Conservative 0; Mismatches 224; Indels 3;
                                 595 GTTGTTGGTGGGGTCCTCCTTCTGGTGGTCGCAGT 629
                                                                                              603
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                                                                                                                                                                                          543 AAGGTGCCCTACAAAGGCATTATGTTATCACTCGTCATGGTTCTCATTCCTTGCGCCATA 602
                                                                                                                                                                                                                                             475
                                                                                                                                                                                                                                                                                                                       418 ATGATGCCACTCTGCATTTATCTCTACACCT---GGTCCTGGAGTCTTCAGCAGAATCTC 474
                                                                                                                                                                                                                                                                                                                                                                                    423 AAGGGGGACATGAACCTCAGCATNGTGATGACCACCTGCTCCAGCTTCACTGCCTTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                          358 GATGGAGATATGGATCTGAGCATCAGTATGACAACCTGTTCCACCGTGGCCGCCCTGGGA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 GTTCTCATCATGGGCTGCCCGGGGGGGCACCATCTCTAACATTTTCACCTTCTGGGTT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 CCCCTCAGTGCTTTCCTTCTGGGCAAGGTCTTTCATCTGACCAGCATTGAGGCTCTGGCC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 CCTTTTACAGCTTATCTCCTGGCCATTAGCTTTTCTCTGAAGCCAGTCCAAGCTATTGCT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 TCGCACATCAGGAGACCCTGGGGGCATTGCTGTGGGACTGCTCTGCCAGTTTTGGGCTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 GTGATGATGGGGCTCATGTTCTCTTTGGGATGTTCCGTGGAGATCCGGAAGCTGTGG
663 ATCATCACTTTCTCCCTCTCTGTGGCTGTCACAGT 697
                                                                                                                                                                                                                                                                                           483 ATGATGCCTCTCCTCTTATACATCTACAGCAAAGGAATCTACGACGGAGATCTTAAGGAC 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 ATCCTCATCTGCGGCTGCTCTCGGGGGGAACCTGTCTAACCTCTTCACCCTGGCCATG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 GCTCACTTCTGGAAGCCCCAAAGGGGTGATCATCGCCCATAGTGGCCCCAGTACGGTATCATG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 GTTATGTTGCTGCTCATCATGCTCTCGCTTGGCTGCACCATGGAGTTCAGCAAGATCAAG 242
                                                                                                                                                                                                                                        GGTGTCTATIGTGAATTACAGATIGGCCAAAACAATCCAAAAATCATTCTCAAGATTGGGGCC
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Technologies. Note: this is a NCI_CGAP Library."
a 265 c 222 g 198 t 1 others
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Search completed: June 9, 2003, 07:06:01 Job time: 1872 secs